10062857

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Term: l1 and (random near5 primer$1 near5 region$1)

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DATE: Monday, May 10, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L3	l1 and (random near5 primer$1 near5 region$1)	1	L3
L2	L1 and random hexamer$1	11	L2
L1	transcrib$7 near5 RNA polymerase near5 cDNA	75	L1

END OF SEARCH HISTORY

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```
=> s random (10A) primer (10a) (ynthesi#### or produc###) RNA
MISSING OPERATOR RODUC###) RNA
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s random (10A) primer# (10a) (synthesi#### or produc###)(10a)RNA
L11          83 RANDOM (10A) PRIMER# (10A) (SYNTHESI#### OR PRODUC###)(10A) RNA

=> s l11 and promoter ans RNA polymerase#
L12           0 L11 AND PROMOTER ANS RNA POLYMERASE#

=> s l11 and promoter# and RNA polymerase#
L13           1 L11 AND PROMOTER# AND RNA POLYMERASE#

=> d l13 bib ab kwic

L13  ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   1991:478216  BIOSIS
DN   PREV199192111976; BA92:111976
TI   EXPRESSION OF A GENERAL TRANSCRIPTION INITIATION FACTOR HTFIID GENE IN
     NORMAL HUMAN TISSUE A QUANTITATIVE ASSAY FOR HTFIID MESSENGER RNA BASED ON
     POLYMERASE CHAIN REACTION PCR.
AU   WADA C [Reprint author]; OHTANI H
CS   DEP CLINICAL PATHOL, SCH MED, KITASATO UNIV, 1-15-1 KITASATO, SAGAMIHARA
     228, JPN
SO   Japanese Journal of Electrophoresis, (1991) Vol. 35, No. 4, pp. 285-290.
     CODEN: SBBKA4. ISSN: 0031-9082.
DT   Article
FS   BA
LA   ENGLISH
ED   Entered STN: 26 Oct 1991
     Last Updated on STN: 26 Oct 1991
AB   A general transcription factor IID (TFIID) binds to the TATA box
     promoter element and regulates the expression of most eukaryotic
     genes transcribed by RNA polymerase II (Pol II).  A
     highly sensitive, specific and quantitative assay for human TFIID (hTFIID)
     mRNA was developed based on polymerase chain reaction (PCR).  The
     distinctive points of our procedure include the use of small amount of
     total cellular RNA (1 μg), a  random primer
     for cDNA synthesis, β2-microglobulin (β2M) as an
     internal control and calculation of the relative value of hTFIID
     transcript from 32P-incorporation of the co-amplified PCR at different
     cycles.  By this procedure, distribution of the hTFIID gene expression was
     for the first time demonstrated in normal human tissues and the amount of
     hTFIID mRNA was measured.  In some tissues such as liver, fetal lung and
     placenta, moderate levels of hTFIId mRNA were detected. hTFIID transcript
     appeared correlated to total mRNA initiation and protein synthesis in
     tissue.  This quantitative PCR procedure can be applied to more extensive
     studies of gene expression.
AB   A general transcription factor IID (TFIID) binds to the TATA box
     promoter element and regulates the expression of most eukaryotic
     genes transcribed by RNA polymerase II (Pol II).  A
     highly sensitive, specific and quantitative assay for human TFIID (hTFIID)
     mRNA was developed based on polymerase chain reaction (PCR).  The
     distinctive points of our procedure include the use of small amount of
     total cellular RNA (1 μg), a  random primer
     for cDNA synthesis, β2-microglobulin (β2M) as an
     internal control and calculation of the relative value of hTFIID
     transcript from 32P-incorporation of the co-amplified.  .  .


=> s l11 and hexamer#
L14          26 L11 AND HEXAMER#
```

=> s l14 and RNA polymerase#
L15 2 L14 AND RNA POLYMERASE#

=> d l15 1-2 bib ab kwic

L15 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:865630 CAPLUS
DN 123:250816
TI Differential display of tissue-specific messenger RNAs in Porphyra perforata (Rhodophyta) thallus
AU Hong, Yong-Ki; Sohn, Chul Hyun; Polne-Fuller, Miriam; Gibor, Aharon
CS Department Biotechnology, National Fisheries University Pusan, Pusan, 608-737, S. Korea
SO Journal of Phycology (1995), 31(4), 640-3
CODEN: JPYLAJ; ISSN: 0022-3646
PB Phycological Society of America
DT Journal
LA English
AB Various tissue-specific markers in differentiated regions of the Porphyra perforata J. Agardh thallus were identified by comparing the differential display derived from the **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue, vegetative non-dividing tissue, and holdfast tissue. First-strand cDNA was **synthesized** by reverse transcription of total **RNA** with **random hexamers** and amplified by PCR with arbitrary **primers**. The morphol. distinct regions of the differentiated tissue revealed the presence of tissue-specific differential display of gene expression.
AB Various tissue-specific markers in differentiated regions of the Porphyra perforata J. Agardh thallus were identified by comparing the differential display derived from the **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue, vegetative non-dividing tissue, and holdfast tissue. First-strand cDNA was **synthesized** by reverse transcription of total **RNA** with **random hexamers** and amplified by PCR with arbitrary **primers**. The morphol. distinct regions of the differentiated tissue revealed the presence of tissue-specific differential display of gene expression.

L15 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1995:453764 BIOSIS
DN PREV199598468064
TI Differential display of tissue-specific messenger RNAs in Porphyra perforata (Rhodophyta) thallus.
AU Hong, Yong-Ki [Reprint author]; Sohn, Chul Hyun; Polne-Fuller, Miriam; Gibor, Aharon
CS Dep. Biotechnol., Natl. Fisheries Univ. Pusan, Nam-ku, Pusan, 608-737, South Korea
SO Journal of Phycology, (1995) Vol. 31, No. 4, pp. 640-643.
CODEN: JPYLAJ. ISSN: 0022-3646.
DT Article
LA English
ED Entered STN: 27 Oct 1995
Last Updated on STN: 27 Oct 1995
AB Various tissue-specific markers in differentiated regions of the Porphyra perforata J. Agardh thallus were identified by comparing the differential display derived from **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue,

vegetative non-dividing tissue, and holdfast tissue. First-strand cDNA was **synthesized** by reverse transcription of total **RNA** with **random hexamers** and amplified by PCR with arbitrary **primers**. The morphologically distinct regions of the differentiated tissue revealed the presence of tissue-specific differential display of gene expression.

AB. . . markers in differentiated regions of the Porphyra perforata J. Agardh thallus were identified by comparing the differential display derived from **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue, vegetative non-dividing tissue, and holdfast tissue. First-strand cDNA was **synthesized** by reverse transcription of total **RNA** with **random hexamers** and amplified by PCR with arbitrary **primers**. The morphologically distinct regions of the differentiated tissue revealed the presence of tissue-specific differential display of gene expression.

IT Miscellaneous Descriptors
GENE EXPRESSION; REGIONAL MARKERS; **RNA POLYMERASE** CHAIN REACTION

L10 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:154562 CAPLUS
DN 138:182030
TI Methods and kits for generating cDNA probes for use in microarrays
IN Hjalt, Tord
PA Curagen Corporation, USA
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003016483	A2	20030227	WO 2002-US26063	20020816

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-312893P P 20010816
AB A novel method of labeling cDNA for probing oligo-based microarrays is disclosed. The polynucleotide template of interest is reverse **transcribed** into double-stranded **cDNA** using **random primers** that include an **RNA** polymerase **promoter**. This cDNA is then used as a template for synthesis of labeled **RNA** via in vitro transcription in the presence of labeled precursors.
AB A novel method of labeling cDNA for probing oligo-based microarrays is disclosed. The polynucleotide template of interest is reverse **transcribed** into double-stranded **cDNA** using **random primers** that include an **RNA** polymerase **promoter**. This cDNA is then used as a template for synthesis of labeled **RNA** via in vitro transcription in the presence of labeled precursors.
IT **Promoter** (genetic element)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(primers hybridizing to **RNA** polymerase; methods and kits for generating cDNA probes for use in microarrays)
IT 9014-24-8
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(phage T7, phage T3 or Sp6, primers hybridizing to **promoters** of; methods and kits for generating cDNA probes for use in microarrays)

L10 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 1
AN 97411082 MEDLINE
DN PubMed ID: 9266104
TI Expression of the prolactin gene in normal and neoplastic human breast tissues and human mammary cell lines: **promoter** usage and alternative mRNA splicing.
AU Shaw-Bruha C M; Pirrucello S J; Shull J D
CS Eppley Institute for Research in Cancer and Allied Diseases, Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha 68198-6805, USA.
NC CA-36727 (NCI)
CA-68529 (NCI)
HD-24189 (NICHD)
SO Breast cancer research and treatment, (1997 Jul) 44 (3) 243-53.

Journal code: 8111104. ISSN: 0167-6806.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U75583
EM 199710
ED Entered STN: 19971013
Last Updated on STN: 19990129
Entered Medline: 19971002
AB Prolactin (PRL) has been implicated in the development of mammary cancer in rodents and humans. Although PRL and its mRNA have been detected in breast tissues and some mammary cell lines, the role of PRL as an autocrine/paracrine growth factor within the breast is not clear. A second, more distal, **promoter** has recently been identified in the human PRL gene. We have used reverse transcription-polymerase chain reaction (RT-PCR) to determine whether the distal or the proximal **promoter** directs expression of the PRL gene in normal and neoplastic breast tissues and in mammary cell lines. Total **RNA** was isolated from 10 normal and 20 neoplastic breast tissue samples and from 8 mammary cell lines; MDA-MB-231, SK-BR-3, T-47D, MCF10, MCF10T2, and 3 MCF7 derivatives. The **RNA** was reverse **transcribed** to **cDNA** using **random** hexamers as **primers**. PCR amplification of the cDNAs was performed, using a variety of PRL-specific primer pairs, and the DNA products were subjected to agarose gel electrophoresis and Southern blotting. The resulting data indicate that the PRL gene is expressed in the majority of both normal and neoplastic breast tissue samples, as well as all of the mammary cell lines. PRL-specific PCR products corresponding to transcripts that originated from the distal **promoter** were observed in a subset of the normal and neoplastic breast tissue samples and mammary cell lines. Together these data indicate that PRL transcripts in human breast tissues and human mammary cell lines originate, at least in part, from the distal PRL **promoter**. In addition, data are presented which suggest that PRL transcripts in breast tissues and mammary cell lines may undergo alternative splicing.
TI Expression of the prolactin gene in normal and neoplastic human breast tissues and human mammary cell lines: **promoter** usage and alternative mRNA splicing.
AB . . . lines, the role of PRL as an autocrine/paracrine growth factor within the breast is not clear. A second, more distal, **promoter** has recently been identified in the human PRL gene. We have used reverse transcription-polymerase chain reaction (RT-PCR) to determine whether the distal or the proximal **promoter** directs expression of the PRL gene in normal and neoplastic breast tissues and in mammary cell lines. Total **RNA** was isolated from 10 normal and 20 neoplastic breast tissue samples and from 8 mammary cell lines; MDA-MB-231, SK-BR-3, T-47D, MCF10, MCF10T2, and 3 MCF7 derivatives. The **RNA** was reverse **transcribed** to **cDNA** using **random** hexamers as **primers**. PCR amplification of the cDNAs was performed, using a variety of PRL-specific primer pairs, and the DNA products were subjected. . . as well as all of the mammary cell lines. PRL-specific PCR products corresponding to transcripts that originated from the distal **promoter** were observed in a subset of the normal and neoplastic breast tissue samples and mammary cell lines. Together these data. . . PRL transcripts in human breast tissues and human mammary cell lines originate, at least in part, from the distal PRL **promoter**. In addition, data are presented which suggest that PRL transcripts in breast tissues and mammary cell lines may undergo alternative. . .
CT . . .
Cloning, Molecular
DNA, Complementary: CH, chemistry
Gene Expression
Molecular Sequence Data

Polymerase Chain Reaction
*Prolactin: GE, genetics
Prolactin: ME, metabolism
***Promoter Regions (Genetics)**
***RNA, Messenger: AN, analysis**
CN 0 (DNA, Complementary); 0 (**RNA**, Messenger)

L10 ANSWER 3 OF 3 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
AN 97081758 EMBASE
DN 1997081758
TI Multiprimed cDNA synthesis followed by PCR is the most suitable method for Epstein-Barr virus transcript analysis in small lymphoma biopsies.
AU Brink A.A.T.P.; Oudejans J.J.; Jiwa M.; Walboomers J.M.M.; Meijer C.J.L.M.; Van den Brule A.J.C.
CS A.J.C. Van den Brule, Section of Molecular Pathology, Department of Pathology, Vrije Universiteit Hospital, De Boelelaan 1117, 1081 HV Amsterdam, Netherlands
SO Molecular and Cellular Probes, (1997) 11/1 (39-47).
Refs: 30
ISSN: 0890-8508 CODEN: MCPRE6
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
005 General Pathology and Pathological Anatomy
016 Cancer
022 Human Genetics
025 Hematology
LA English
SL English
AB In this study, the reverse transcriptase-polymerase chain reaction (RT-PCR) for the reliable detection of multiple Epstein-Barr virus (EBV) transcripts was optimized and subsequently evaluated on lymphoma specimens. Since often only small lymphoma biopsies are available for analysis of EBV **transcripts**, several RT-protocols to generate **cDNA** from multiple targets were applied. These were multi-**primer**, oligo-dT primed and **random** hexamer primed cDNA synthesis. Multi-primer cDNA synthesis appeared to be the most suitable method for subsequent PCR analysis of EBV targets; simultaneous priming with up to 10 specific antisense primers (for EBNA1 and 2, LMP1 and 2, BARF0, BHRF1, BZLF1, C **promoter** activity and the **RNA** control genes U1A and c-abl) followed by PCR showed no loss of sensitivity compared to single-specific antisense priming. Transcripts were specifically detected in up to one EBV-positive JY cell in a background of 50,000 EBV-negative BJAB cells, with the exception of BZLF1 and QK spliced EBNA1 transcripts which could only be detected in 1000 and 10,000 EBV-positive cells, respectively. The analytical sensitivities of all the primers used in PCR, including BZLF1 and QK EBNA1 primers, were 1-10 copies of cloned RT-PCR products. The multi-primed RT-PCR was evaluated on lymphomas (n = 13). In cases with proper **RNA** quality, EBV expression patterns found were identical to those found in previous studies using single-primed RT-PCR assays. In conclusion, this study shows that multi-primed RT-PCR analysis can be used efficiently for EBV transcript analysis in small lymphoma biopsies, thereby facilitating studies concerning the role of EBV in lymphomagenesis.
AB . . . was optimized and subsequently evaluated on lymphoma specimens. Since often only small lymphoma biopsies are available for analysis of EBV **transcripts**, several RT-protocols to generate **cDNA** from multiple targets were applied. These were multi-**primer**, oligo-dT primed and **random** hexamer primed cDNA synthesis. Multi-primer cDNA synthesis appeared to be the most suitable method for subsequent PCR analysis of EBV. . . . simultaneous priming with up to 10 specific antisense primers (for EBNA1 and 2, LMP1 and 2, BARF0, BHRF1, BZLF1, C **promoter** activity and the **RNA** control genes U1A and

c-abl) followed by PCR showed no loss of sensitivity compared to single-specific antisense priming. Transcripts were. . . 1-10 copies of cloned RT-PCR products. The multi-primed RT-PCR was evaluated on lymphomas (n = 13). In cases with proper **RNA** quality, EBV expression patterns found were identical to those found in previous studies using single-primed RT-PCR assays. In conclusion, this. . .

CT Medical Descriptors:
*epstein barr virus
*lymphoma
*reverse transcription polymerase chain reaction
***rna analysis**
article
controlled study
human
human cell
human tissue
nonhuman
priority journal
tumor biopsy
*complementary dna
***virus messenger rna: EC, endogenous compound**
cell nucleus antigen
primer dna